

## SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Katz, Leonard  
Stassi, Diane L.  
Summers Jr., Richard G.  
Ruan, Xiaolan  
Pereda-Lopez, Ana  
Kakavas, Stephan J.

(ii) TITLE OF THE INVENTION: NOVEL POLYKETIDE DERIVATIVES  
AND RECOMBINANT METHODS FOR MAKING SAME

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories  
(B) STREET: 100 Abbott Park Rd.  
(C) CITY: Abbott Park  
(D) STATE: Illinois  
(E) COUNTRY: USA  
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 16-MAY-1979  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dianne Casuto  
(B) REGISTRATION NUMBER: P-40,943  
(C) REFERENCE/DOCKET NUMBER: 4952.US.P2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (847)-938-3137  
(B) TELEFAX: (847)-938-2623  
(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

GGGCCGCTGG CGGTGATGTT CACCGGACAG GGCTCCCAAC GCCCGGGCAT GGGACGACAG      60
TTGTACGAGC ACTTCCCCGT CTTGCCCCAG GCACTGGACG AGGTCTTCGC ACTCGCCACC      120
CCCGGACTAC GCGAGGTGAT GTTCGACCCC GACCAGGCCG AAACACTCCA ACGCACCAGC      180
CACGCCCAGA TCGCCCTGTT CGCCTTCGAA ACCGCCCTCT ACCGACTCTG GGAATCCTGG      240
GGCTTGGGAC CCGACATGGT CTGCGGACAC TCGGTCGGAG AAATCACCAG AGCCCACGTC      300
TCCGGCAGCC TCACCTCCCT CGACGCCGTC CACCTCGTCA CCACACGCGG CACCCTCATG      360
CAAAACCTGC CCCCCGGCGG CGCATGCTC GCCGTGCGCA CCGACCCCCA CACCCTCCAA      420
CCCCACCTCG ACAACCACCA CGACACCATC TCCATCGCCG CCATCAACGG CCCCCACGCC      480
ACCGTCTCTT CCGGCGACCG CACCACCTTC CACCACATCG CCACCCAAC T CAACACCAA      540
CCCTTCACCA CCACCTCAA CACCCTCACC CACCACCCCC CACACACACC CCTCATCAGC      600
ATGCTCACCG CCACACCCAC CCACCCCGAC ACCACCCACT GGACCCAGCA CATCACCGCA      660
CCCGTCCGCT ACACCGACAC CCTCCACCAC CTCACACCACC ACGGCATCAC CACCTACCTC      720
GAAATCGGCC CCGACACCAC CCTCACCGCC CTCGCCCGCA CCACCTCCCT CACCACCACC      780
CACCTCATCC CCACCACCCG CCGCAACCAC AACGAAGTCC GCAGCACGAA CGAGGCGTTG      840
GGCAGGGTGT TCAGCGTGGG CCACTCGGTG GACTGGCGGG CCTCACTCC GACCGGGAGG      900
CGTACCTCCC TGCCGACGTA CCCCCT                                     925

```

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

CCTAGGACGG CAGTCTTGCT CACCGGGCAG GGTTCACGAC GTCAGGGCAT GGGGCGCGAA      60
CTGTACGACC GGTACCCGGT GTTCGCCGCC TCGTTGACAG CGATCTGCGC TCAACTCGAC      120
GGGCAACTGC CTCGTCCCCT CAAGGACGTT CTCCTCGCCC CCGAGGGGTC GGAGGACGCC      180
GCGCTCATCG ACCGTACGGT GTTCACACAG GCGGCTCTGT TCGCCGTGGA GACCTCCCTG      240
TTCCGGCTGT TCGAGGCCCA CGGCCTCGTC CCCGACTACC TCATCGGCCA CTCCATCGGC      300
GAAGTGACCG CGGCCACCT GGCCGGGGTC CTCGATCTGG CGGACGCGTG CGTCCTGGTC      360
GCCCACCGCG GCCGCTGAT GCAGTCGGCC CGGGCCGGCG GCGCGATGGC CGCGGTCCAG      420
GCGAGCGAGG ACGAGGTACG CGAGGCCCTC GCGACCTTCG ACGATGCGGT TGCCGTGGCC      480
GGAGTCAACG GCCCGAACGC CACCGTCGTC TCCGCGACAG AGGACGCGGT CGAGCGGCTG      540
GTCGCGCGCT GCGCGGAGCA GGGCAGGCGG ACGAAGCGGC TGCCGGTCAG CCACGCCTTC      600
CACTCGCCGC ACATGGACGG GATCGTCGAC GAGTTCGTCA CCGCCGTCTC CGGGCTCACC      660
TTCCGCTCCC CGACGATCCC GGTGCTCTCC AACGTACCG GGACCCTCGC CACCGTCGAC      720
CAGCTGACCT CGCCGCGGTA CTGGGACGCG CACATCCGCG AGGCCGTGCG CTTCGCCGAC      780
GGGGTGCGGT ACCTGGAGGG CGAGGGCGTC ACCGAATGGC TGGAGCTCGG GCCCGACGGC      840

```

09735056.12100

GTTCTCGTCG CCCTGGTCTGA GGACTGCCTG GCGAAGGAGG CGGGATCGCT CGCGTCCGCC 900  
 CTGCGCAAGG GGGCGAGCGA GCCCCACACC GTGGGCGCGG CCATGGCCCG CGCGGTGCTG 960  
 CGCGGATCCG GCCCCGACTG GGCGGCGGTG TTCCCCGGCG CACGGCGGGT CGACCTTCCG 1020  
 ACGTATGCAT 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATCTACACST CSGGCACSAC SGGCAAGCCS AAGGG 35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTSAAGGCSG GCGGCGCSTA CGTSCCSATC GACCC 35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCGAATTCC TAGGCTGGCG GTGATGTTCA 30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

00121" 9505269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCCGGATCCA TGCATACGTC GGCAGGGAGG TAC

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTCGAATTC GCTGGTCGCG GTGCACCT

28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACGGATCCG GCCCTAGGCT GCGCCCGGCT CG

12

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGGGATCCT ATGCATTCCA GCGCGAGCGC

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

00735056-12100

26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

36

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

42

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

36

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCGAATTC CCTAGGACGG CAGTCCTGCT CACC

34

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGGATCC ATGCATACGT CGGAAGGTCG ACCCG

35

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCGAAGAAT TCCCTAGGGT TGCCTTCCTG TTCGAC

36

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCGAAAAGC TTATGCATAG ACCGGCAGAT CCACCG

36

## (2) INFORMATION FOR SEQ ID NO:19:

09735055 131100

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGGTTAAGTC SAACATCGG

19

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCRATCTCRC CCTGCGARTG

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGAGAGGAA CCAACGCGCA CGTGATCGTC GAAGAGGCAC CAGC

44

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAGAGAGGAT CCGACCTAGG CGCGGAGGTC ACCGGCGCGA CGGCCG

45

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

001121 990940

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAGAGACCTA GGAAGCCGGT GTTCGTGTTC CCCGGCCAGG GCT

43

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGAGAGGAT CCGAGGCCGG CCGTGC GCCC GGACCGAAGA CCGCCTC

47

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGAGAATTC CCTAGGGTCG CTTTCGTCTT TCCCGGGCAG G

41

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTGAGATCTT ATGCATACGA GGGAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs

09735056 121100



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTGAGATCTT ATGCATACGA GGGAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTGAGATCTT ATGCATACGA GGGAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1010 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCCGACCGTG	TCGTGTTCTG	GTTCCCCGGC	CAGGGCTCGC	AGTGGGCCGG	AATGGCCGAG	60
GGGCTGCTGG	AGCGGTCCGG	CGCGTTCCGG	AGTGGGCCGG	ACTCGTGCGA	CGCCGCGCTG	120
CGGCCGTACC	TCGGCTGGTC	GGTGTGAGC	GTGCTGCGCG	GGGAACCGGA	CGCGCCCTCG	180
CTCGACCGGG	TCGACGTCGT	GCAGCCGGTG	CTGTTACGA	TGATGGTCTC	GCTCGCGGCG	240
GTCTGGCGTG	CGCTGGGGGT	GGAACCGGCG	GCGGTCTGTC	GGCACTCGCA	GGGTGAGATC	300
GCCGCTGCCC	ATGTCGCCGG	TGCGCTGTCT	CTGGACGACT	CGGCCCGGAT	CGTCGCCCTG	360
CGCAGTCGGG	CGTGGCTCGG	ACTGGCGGGC	AAGGGCGGCA	TGGTGGCGGT	GCCGATGCCG	420
GCGGAGGAGC	TGCGGCCGCG	GCTGGTGACG	TGGGGGGACC	GTCTGGCCGT	CGCCGCCGTC	480
AACAGCCCCG	GTTCTTGCGC	CGTCGCAGGC	GACCCGAGAG	CGCTGGCCGA	ACTGGTGGCG	540
CTGCTGACCG	GTGAGGGGGT	GCACGCCCGG	CCGATCCCCG	GCGTCGACAC	GGCGGGCCAC	600
TCGCCGCAGG	TGGACCGGTT	GCGGGCTCAT	CTGCTGGAGG	TGCTGGCCCC	GGTCGCCCCC	660
CGACCGGCCG	ACATCCCGTT	CTACTCGACG	GTGACCGGCG	GGCTGCTGGA	CGGCACCGAG	720
CTGACGCGGA	CGTACTGGTA	CCGCAACATG	CGCGAGCCCG	TCGAGTTCTGA	GCGGGCCACA	780
CGGGCGCTGA	TCGCCGACGG	GCACGACGTC	TTCCTGGAGA	CGAGCCCGCA	TCCCATGCTG	840
GCCGTGGCGC	TGGAGCAGAC	GGTCACCGAC	GCCGGCACC	ACGCGGCGGT	GCTCGGGACC	900
CTGCGCCGCC	GCCACGGCGG	TCCTCGCGCG	CTGGCCCTGG	CCGCTGCGCG	CGCCTTCGCG	960
AGGCGGTCTT	CGGTCCGGGC	GCACGGCCCC	TGGAGTTGCC	CACCTATCCG		1010

(2) INFORMATION FOR SEQ ID NO:30:

09735056-124100

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGCGCGCCTG CCTTCGTCTT TCCCGGGCAG GCGGCCAGT GGGCCGACT GGGAGCGCGG 60  
 CTCCTCGCGG ACTCCCCCGT CTTCCGCGCC AGGGCCGAGG CATGCGCGCG GCGCTGGAG 120  
 CCTCACCTCG ACTGGTCGGT CCTCGACGTG CTGGCCGGCG CCCCGGGCAC CCCTCCCATC 180  
 GACCGGGCCC ACGTGGTGCA GCCGGTGCTG TTCACCACGA TGGTCTCGCT GGCCGCCCTC 240  
 TGGGAGGCCC ACGGGGTGCG GCCGGCCGCG GTCGTGGGCC ACTCCAGGG CGAGGTGGCC 300  
 GCGGCCTGCG TGGCCGGTGC CCTGTGCTG GACGACGCTG CCCTGGTGAT CGCCGGACGC 360  
 AGCAGGCTGT GGGGGCGGCT GGCCGGGAAC GCGGGGATGC TCGCGGTGAT GGCTCCGGCC 420  
 GAGCGGATCC GTGAGCTGCT CGAACCATGG CCGCAGCGGA TTTCGGTGGC GCGGGTCAAT 480  
 GGCCCCGCCT CGGTACCGT CTCCGGTGAC GCGCTCGCGC TGGAGGAGTT CGGCGCGCGG 540  
 CTCTCCGCCG AGGGGGTGCT GCGCTGGCCG CTGCCGGGCG TCGACTTCGC CGGCCACTCG 600  
 CCGCAGGTGG AGGAGTTCCG CGCTGAGCTC CTGGACCTGC TCTCCGGCGT ACGGCCGGCT 660  
 CCTTCGCGGA TACCTTTCTT CTCCACCGTG ACGGCGGGTC CTTGCGGCGG CGACCAGCTG 720  
 GACGGGGCGT ACTGGTACCG CAACACGCGC GAACCCGTGG AGTTCGACGC CACGGTCCGG 780  
 GCGCTGCTGC GTGCGGGCCA TCACACGTTT ATCGAGGTGC GTCCGCATCC GCTGCTCAAC 840  
 GCCGCGATCG ACGAGATCGC AGCGGACGAG GGGGTAGCGG CCACGGCCCT GCATACGCTC 900  
 CAGCGGGGCG CTGGCGGCC TGAACGCGTG CGCAACGCGG TGGGCGCCG TTTGCGGCAC 960  
 GGTTCGCGG TCGACTGGAA CGCCCTGTTT GAGGGCACCG GTGCGGCGAG GGTGCCGCTT 1020  
 CCCTCGTACG CCTTC 1035

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Pro Leu Ala Val Met Phe Thr Gly Gln Gly Ser Gln Arg Pro Gly  
 1 5 10 15  
 Met Gly Arg Gln Leu Tyr Glu His Phe Pro Val Phe Ala Gln Ala Leu  
 20 25 30  
 Asp Glu Val Phe Ala Leu Ala Thr Pro Gly Leu Arg Glu Val Met Phe  
 35 40 45  
 Asp Pro Asp Gln Ala Glu Thr Leu Gln Arg Thr Asp His Ala Gln Ile  
 50 55 60  
 Ala Leu Phe Ala Phe Glu Thr Ala Leu Tyr Arg Leu Trp Glu Ser Trp  
 65 70 75 80  
 Gly Leu Arg Pro Asp Met Val Cys Gly His Ser Val Gly Glu Ile Thr  
 85 90 95  
 Ala Ala His Val Ser Gly Thr Leu Thr Leu Pro Asp Ala Val His Leu

100 105 110  
 Val Thr Thr Arg Gly Thr Leu Met Gln Asn Leu Pro Pro Gly Gly Ala  
 115 120 125  
 Met Leu Ala Val Ala Thr Asp Pro His Thr Leu Gln Pro His Leu Asp  
 130 135 140  
 Asn His His Asp Thr Ile Ser Ile Ala Ala Ile Asn Gly Pro His Ala  
 145 150 155 160  
 Thr Val Leu Ser Gly Asp Arg Thr Thr Leu His His Ile Ala Thr Gln  
 165 170 175  
 Leu Asn Thr Lys Thr Asn Trp Leu Asn Val Ser His Ala Phe His Ser  
 180 185 190  
 Pro Leu Met Gln Pro Ile Leu Gln Pro Phe Thr Thr Thr Leu Asn Thr  
 195 200 205  
 Leu Thr His His Pro Pro His Thr Pro Leu Ile Ser Met Leu Thr Ala  
 210 215 220  
 Thr Pro Thr His Pro Asp Thr Thr His Trp Thr Gln His Ile Thr Ala  
 225 230 235 240  
 Pro Val Arg Tyr Thr Asp Thr Leu His His Leu His His His Gly Ile  
 245 250 255  
 Thr Thr Tyr Leu Glu Ile Gly Pro Asp Thr Thr Leu Thr Ala Leu Ala  
 260 265 270  
 Arg Thr Thr Leu Pro Thr Thr Thr His Leu Ile Pro Thr Thr Arg Arg  
 275 280 285  
 Asn His Asn Glu Val Arg Ser Thr Asn Glu Ala Leu Gly Arg Val Phe  
 290 295 300  
 Ser Val Gly His Ser Val Asp Trp Arg Ala Leu Thr Pro Thr Gly Arg  
 305 310 315 320  
 Arg Thr Ser Leu Pro Thr Tyr Pro  
 325

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro Arg Thr Ala Val Leu Leu Thr Gly Gln Gly Ser Gln Arg Gln Gly  
 1 5 10 15  
 Met Gly Arg Glu Leu Tyr Asp Arg Ser Pro Val Phe Ala Ala Ser Phe  
 20 25 30  
 Asp Ala Ile Cys Ala Gln Leu Asp Gly Gln Leu Pro Arg Pro Leu Lys  
 35 40 45  
 Asp Val Leu Phe Ala Pro Glu Gly Ser Glu Asp Ala Ala Leu Ile Asp  
 50 55 60  
 Arg Thr Val Phe Thr Gln Ala Ala Leu Phe Ala Val Glu Thr Ser Leu  
 65 70 75 80  
 Phe Arg Leu Phe Glu Ala His Gly Leu Val Pro Asp Tyr Leu Ile Gly

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85 90 95  
 His Ser Ile Gly Glu Val Thr Ala Ala His Leu Ala Gly Val Leu Asp  
 100 105 110  
 Leu Ala Asp Ala Cys Val Leu Val Ala His Arg Gly Arg Leu Met Gln  
 115 120 125  
 Ser Ala Arg Ala Gly Gly Ala Met Ala Ala Val Gln Ala Ser Glu Asp  
 130 135 140  
 Glu Val Arg Glu Ala Leu Ala Thr Phe Asp Asp Ala Val Ala Val Ala  
 145 150 155 160  
 Gly Val Asn Gly Pro Asn Ala Thr Val Val Ser Gly Asp Glu Asp Ala  
 165 170 175  
 Val Glu Arg Leu Val Ala Arg Trp Arg Glu Gln Gly Arg Arg Thr Lys  
 180 185 190  
 Arg Leu Pro Val Ser His Ala Phe His Ser Pro His Met Asp Gly Ile  
 195 200 205  
 Val Asp Glu Phe Val Thr Ala Val Ser Gly Leu Thr Phe Arg Ser Pro  
 210 215 220  
 Thr Ile Pro Val Val Ser Asn Val Thr Gly Thr Leu Ala Thr Val Asp  
 225 230 235 240  
 Gln Leu Thr Ser Pro Ala Tyr Trp Ala Arg His Ile Arg Glu Ala Val  
 245 250 255  
 Arg Phe Ala Asp Gly Val Arg Tyr Leu Glu Gly Glu Gly Val Thr Glu  
 260 265 270  
 Trp Leu Glu Leu Gly Pro Asp Gly Val Leu Val Ala Leu Val Glu Asp  
 275 280 285  
 Cys Leu Ala Lys Glu Ala Gly Ser Leu Ala Ser Ala Leu Arg Lys Gly  
 290 295 300  
 Ala Ser Glu Pro His Thr Val Gly Ala Ala Met Ala Arg Ala Val Leu  
 305 310 315 320  
 Arg Gly Ser Gly Pro Asp Trp Ala Ala Val Phe Pro Gly Ala Arg Arg  
 325 330 335  
 Val Asp Leu Pro Thr Tyr Ala  
 340

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Asp Arg Val Val Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Ala  
 1 5 10 15  
 Gly Met Ala Glu Gly Leu Leu Glu Arg Ser Gly Ala Phe Arg Ser Ala  
 20 25 30  
 Ala Asp Ser Cys Asp Ala Ala Leu Arg Pro Tyr Leu Gly Trp Ser Val  
 35 40 45  
 Leu Ser Val Leu Arg Gly Glu Pro Asp Ala Pro Ser Leu Asp Arg Val

09735056 121100

50 55 60  
 Asp Val Val Gln Pro Val Leu Phe Thr Met Met Val Ser Leu Ala Ala  
 65 70 75 80  
 Val Trp Arg Ala Leu Gly Val Glu Pro Ala Ala Val Val Gly His Ser  
 85 90 95  
 Gln Gly Glu Ile Ala Ala Ala His Val Ala Gly Ala Leu Ser Leu Asp  
 100 105 110  
 Asp Ser Ala Arg Ile Val Ala Leu Arg Ser Arg Ala Trp Leu Gly Leu  
 115 120 125  
 Ala Gly Lys Gly Gly Met Val Ala Val Pro Met Pro Ala Glu Glu Leu  
 130 135 140  
 Arg Pro Arg Leu Val Thr Trp Gly Asp Arg Leu Ala Val Ala Ala Val  
 145 150 155 160  
 Asn Ser Pro Gly Ser Cys Ala Val Ala Gly Asp Pro Glu Ala Leu Ala  
 165 170 175  
 Glu Leu Val Ala Leu Leu Thr Gly Glu Gly Val His Ala Arg Pro Ile  
 180 185 190  
 Pro Gly Val Asp Thr Ala Gly His Ser Pro Gln Val Asp Ala Leu Arg  
 195 200 205  
 Ala His Leu Leu Glu Val Leu Ala Pro Val Ala Pro Arg Pro Ala Asp  
 210 215 220  
 Ile Pro Phe Tyr Ser Thr Val Thr Gly Gly Leu Leu Asp Gly Thr Glu  
 225 230 235 240  
 Leu Asp Ala Thr Tyr Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe  
 245 250 255  
 Glu Arg Ala Thr Arg Ala Leu Ile Ala Asp Gly His Asp Val Phe Leu  
 260 265 270  
 Glu Thr Ser Pro His Pro Met Leu Ala Val Ala Leu Glu Gln Thr Val  
 275 280 285  
 Thr Asp Ala Gly Thr Asp Ala Ala Val Leu Gly Thr Leu Arg Arg Arg  
 290 295 300  
 His Gly Gly Pro Arg Ala Leu Ala Leu Ala Val Cys Arg Ala Phe Ala  
 305 310 315 320  
 His Gly Val Glu Val Asp Pro Glu Ala Val Phe Gly Pro Gly Ala Arg  
 325 330 335  
 Pro Val Glu Leu Pro Thr Tyr Pro  
 340

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Ala Pro Ala Phe Val Phe Pro Gly Gln Gly Ala Gln Trp Ala Gly  
 1 5 10 15  
 Leu Gly Ala Arg Leu Leu Ala Asp Ser Pro Val Phe Arg Ala Arg Ala

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20						25					30				
Glu	Ala	Cys	Ala	Arg	Ala	Leu	Glu	Pro	His	Leu	Asp	Trp	Ser	Val	Leu
35						40					45				
Asp	Val	Leu	Ala	Gly	Ala	Pro	Gly	Thr	Pro	Pro	Ile	Asp	Arg	Ala	Asp
50						55					60				
Val	Val	Gln	Pro	Val	Leu	Phe	Thr	Thr	Met	Val	Ser	Leu	Ala	Ala	Leu
65						70					75				
Trp	Glu	Ala	His	Gly	Val	Arg	Pro	Ala	Ala	Val	Val	Gly	His	Ser	Gln
85						90					95				
Gly	Glu	Val	Ala	Ala	Cys	Val	Ala	Gly	Ala	Leu	Ser	Leu	Asp	Asp	
100						105					110				
Ala	Ala	Leu	Val	Ile	Ala	Gly	Arg	Ser	Arg	Leu	Trp	Gly	Arg	Leu	Ala
115						120					125				
Gly	Asn	Gly	Gly	Met	Leu	Ala	Val	Met	Ala	Pro	Ala	Glu	Arg	Ile	Arg
130						135					140				
Glu	Leu	Leu	Glu	Pro	Trp	Arg	Gln	Arg	Ile	Ser	Val	Ala	Ala	Val	Asn
145						150					155				
Gly	Pro	Ala	Ser	Val	Thr	Val	Ser	Gly	Asp	Ala	Leu	Ala	Leu	Glu	Glu
165						170					175				
Phe	Gly	Ala	Arg	Leu	Ser	Ala	Glu	Gly	Val	Leu	Arg	Trp	Pro	Leu	Pro
180						185					190				
Gly	Val	Asp	Phe	Ala	Gly	His	Ser	Pro	Gln	Val	Glu	Glu	Phe	Arg	Ala
195						200					205				
Glu	Leu	Leu	Asp	Leu	Leu	Ser	Gly	Val	Arg	Pro	Ala	Pro	Ser	Arg	Ile
210						215					220				
Pro	Phe	Phe	Ser	Thr	Val	Thr	Ala	Gly	Pro	Cys	Gly	Gly	Asp	Gln	Leu
225						230					235				
Asp	Gly	Ala	Tyr	Trp	Tyr	Arg	Asn	Thr	Arg	Glu	Pro	Val	Glu	Phe	Asp
245						250					255				
Ala	Thr	Val	Arg	Ala	Leu	Leu	Arg	Ala	Gly	His	His	Thr	Phe	Ile	Glu
260						265					270				
Val	Gly	Pro	His	Pro	Leu	Leu	Asn	Ala	Ala	Ile	Asp	Glu	Ile	Ala	Ala
275						280					285				
Asp	Glu	Gly	Val	Ala	Ala	Thr	Ala	Leu	His	Thr	Leu	Gln	Arg	Gly	Ala
290						295					300				
Gly	Gly	Leu	Asp	Arg	Val	Arg	Asn	Ala	Val	Gly	Ala	Ala	Phe	Ala	His
305						310					315				
Gly	Val	Arg	Val	Asp	Trp	Asn	Ala	Leu	Phe	Glu	Gly	Thr	Gly	Ala	Arg
325						330					335				
Arg	Val	Pro	Leu	Pro	Ser	Tyr	Ala	Phe							
340						345									